

SEQ ID No.	Source Organism	Element Name	Sequence
1	wheat	Em1a	TGCCGGACACGTGGCGCGA
2*	maize	ABRE1	TTCGAGAAGAACCGAGACGTGGCGGGC
3	maize	ABRE A	GCGCTCGCGCCACGTGGGCATGCCGCC
4	maize	Prolamin P-box	GGTTGTCACATGTGTAAAGGTGAAG
5	maize	Z2 and Z3 box	GATCATGCATGTCATTCCACGTAGATAA
6	CaMV	35S AS-2	GTGGATTGATGTGATATCTC
7*	CaMV	35S AS-1 (As-1)	TCCACTGACGTAAGGGATGACGCACAAT
8	<i>Agrobacterium T-DNA</i>	OCS ele	TGACGTAAGCGCTTACGTCA
9	tobacco	GCC-box	GACTAATGGCGGCTCTTATCTCAC
10	soybean	GH3 D1	GCCCTCGTGTCTCTCAATAAGCTA
11	soybean	GH3 D3	GCAATCCTTTGTCTCAATAAGTTCCAC
12	soybean	P3	AAGGGAGACAACTTGTCTCCCA
13	pea	GT-1 rbcS3A	ATCTTGTGTGGTTAATATGGCTGC
14	Arabidopsis	TCA motif	CTTCATCTTCTTCTCCACCAAACG
15	Arabidopsis	C-repeat/DRE	ATTCATGGCCGACCTGCTTTTT
16	soybean	HSE	AGAAGCTTCCAGAAGCTTCTAGAAG
17	maize	ERE	ATGCACGAATTGACCATTCC
18	parsley	gln2 PR box	CATAAGAGCCGCCACTAAAATAAGACCG
19	wheat	HBP-1a	GGCCACGTCACCAATCCGCG
20	maize	A1 PROMOTER	CGGGTCAGTGACCTACCAACCTTAAACAC
21	maize	Bz1 PROMOTER	CGTCTAACTGCGACTGGCAGGTGCGCAC
22	parsley	CHS promoter	ATCCGGTGGCCGTCCCTCCAACCTAACCT
23	rice tungro bacilliform virus	BoxII	CCAGTGTGCCCTGG
24*	rice	phyA GT-2 (GT-2)	TAGGTTAATTATTGGCGGTAATTA
25	synthetic	GT-2 like	AAACGGTAAAAAGCGGTAGATTACC
26	oat	Phy PF1	GAAATAGCAAATGTTAAAAATA
27	soybean	AT-com	AAAAATAATATTAATATTATATTGAAA
28	Arabidopsis	AG site	ATAAGCTTTACCATTAATGGTAAAGCTTGG
29	Arabidopsis	AP3 site	CAATACTTTCCATTTTTAGTAACTAAGCTT
30	Arabidopsis	TGAC motif	GGTATCGTTGACCGAGTTGACT
31	petunia	CAGT motif	TTGACAGTGTCACTTGACAGTGTACAC
32	maize	Dof1/Dof2	GATCAAAAAAGTGAGATC
33	parsley	pr2 oligomer II	ATTCAATAGTGTGCTAATTGTTTAAGAGTTG
34	barley	CE1	TGCCATTGCCACCGGCCCCCA
35	soybean	H-box1	AGCAGACATGGTAGGCAGTGCA
36	bean	H-box2	TCACCTACCCTACTTCCTATCC
37	barley	lox1	AATCGTCATGAATGAAGTCATGTGACGGCT
38	tobacco	PR-2d	AGGGGCAGCTTCGACCTCCTTCTCC
39	synthetic	ROL6	TCAGAACACGCAAGTTGCCAGCTCACCCAAC
40	maize	SGB box 2/3	AGATATGCATGATCTTTAAC
41	maize	SGB box 6-8	TGCGGTTTCTTTTGGCACAAATGGCATGA
42	maize	MS-BS7 box1-3	AAATCTACCTCCAACCAACCCAGCTTTGTA
43	maize	MS-BS7 box22-24	ATCACACCAACTTATCACCTAGAAAAGCGA
44	soybean	AuxRE DR5	CCTTTTGTCTCCCTTTTGTCTC
45*	rice	PCNA IIA	CGAGGTGGGCCCCTAGGTGGGCCCGTAT
46	parsley	PAL1 Box E	TACCTTTTACCCTTCATGTCATC
47	pea	myb26	GTCGACAAAAGTTAGGTTAGCAGGC
48	barley	GARE	GGCCGATAACAAACTCCGGCC
49	tomato	E8	TTTTATTCCCAACAATAGAAAGTCTTG
50	tobacco	E1RE	GATTTGGTCAGAAAGTCAGTCC
51	wheat	CA	GTAGTGCCACCAAAACACAACATACCAAATTA
52	rape	napA	GATCCACATACACATACACG
53	sunflower	HaG3-A -75	CAGCTCCAAATGGTGATCTTCTCCTGG
54	sunflower	HaG3-A -111	TATACAGATGTAGCATGTCT
55	maize	Prolamin box	TTGACGTGTAAAGTAAATTTACAAC
56	pea	TGAC-like	GACACGTAGAATGAGTCATCAC
57	maize	SP20+6	GTCCCTCTCCCGTCCCAGAGAAACCC
58	tobacco	MSA RT1	TGTCCCCCAACGGTCTTATT
59*	Arabidopsis	DRE rd29A1 (DRE 1)	ATATCATACCGACATCAGTT
60	Arabidopsis	DRE rd29A2	ATATACTACCGACATGAGTT
61	Arabidopsis	CGF-1	GATAAAGATTACTTCAGATATAACAAACGTT
62	tobacco	ltp1 D1	TTCCCCTAGCTAGATACTTCATT
63	pea	ENBP1	CGATTATTGAGATATATAATAAATTAG
64	tomato	MRE	CGAAAACATACGCGCGAAATT

Figure 1

# 2-D Pooling of Transcription Factor Binding Sites

( 8 X 8 )

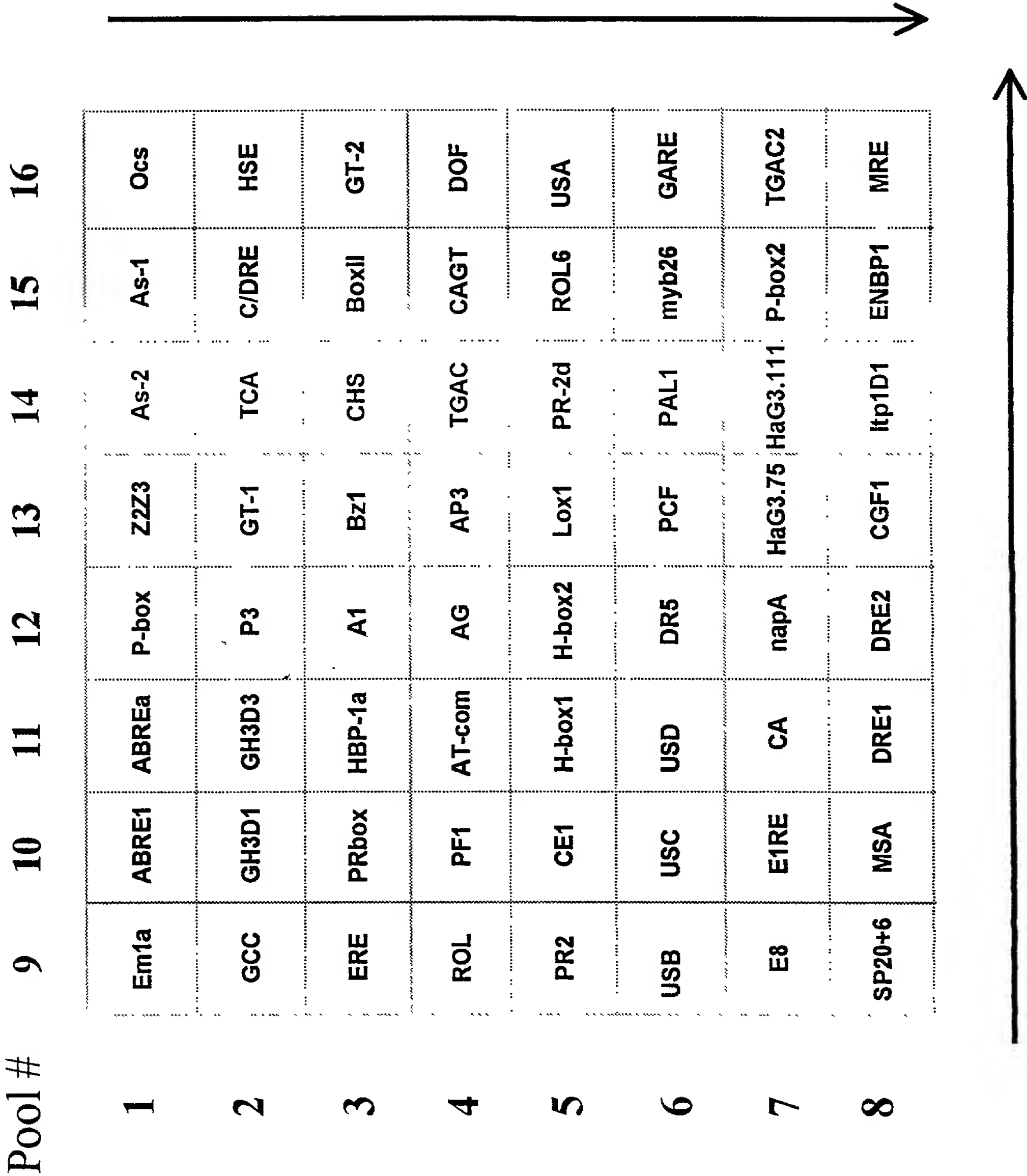


FIGURE 2

# Strong Binding Activities in Maize Nuclear Extracts

9 10 11 12 13 14 15 16

1	Em1a	ABRE1	ABREa	P-box	ZZZ3	As-2	As-1	Ocs
2	GCC	GH3D1	GH3D3	P3	GT-1	TCA	C/DRE	HSE
3	ERE	PRbox	HBP-1a	A1	Bz1	CHS	BoxII	GT-2
4	ROL	PF1	AT-com	AG	AP3	TGAC	CAGT	DOF
5	PR2	CE1	H-box1	H-box2	Lox1	PR-2d	ROL6	USA
6	USB	USC	USD	DR5	PCF	PAL1	myb26	GARE
7	E8	E1RE	CA	napA	HaG3.75	HaG3.111	P-box2	TGAC2
8	SP20+6	MSA	DRE1	DRE2	CGF1	ltp1D1	ENBP1	MRE

FIGURE 3

# Transient Assay for Multimers of Transcription Factor Binding Sites

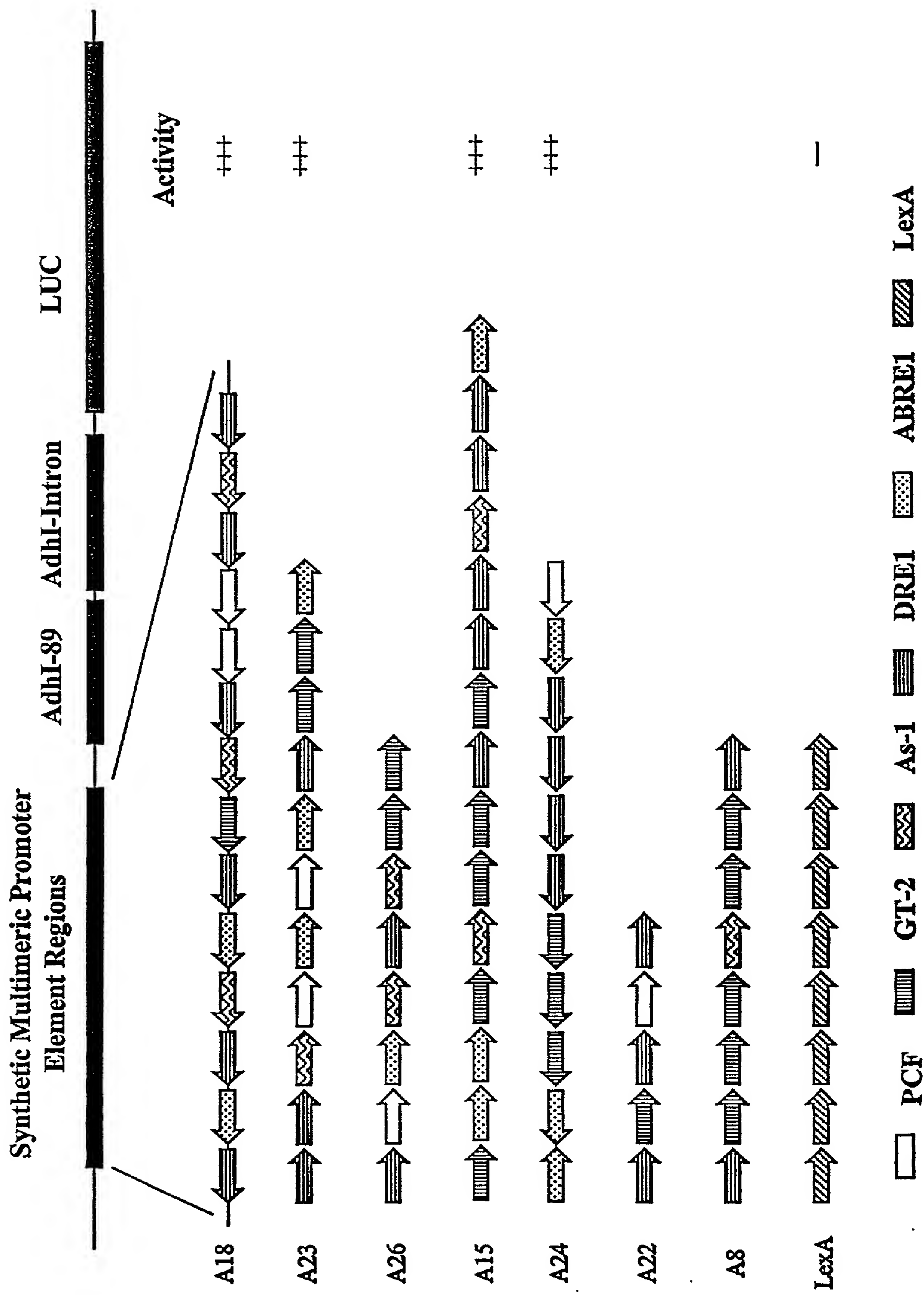


FIGURE 4

# Transient Assay for Multimers of Transcription Factor Binding Sites

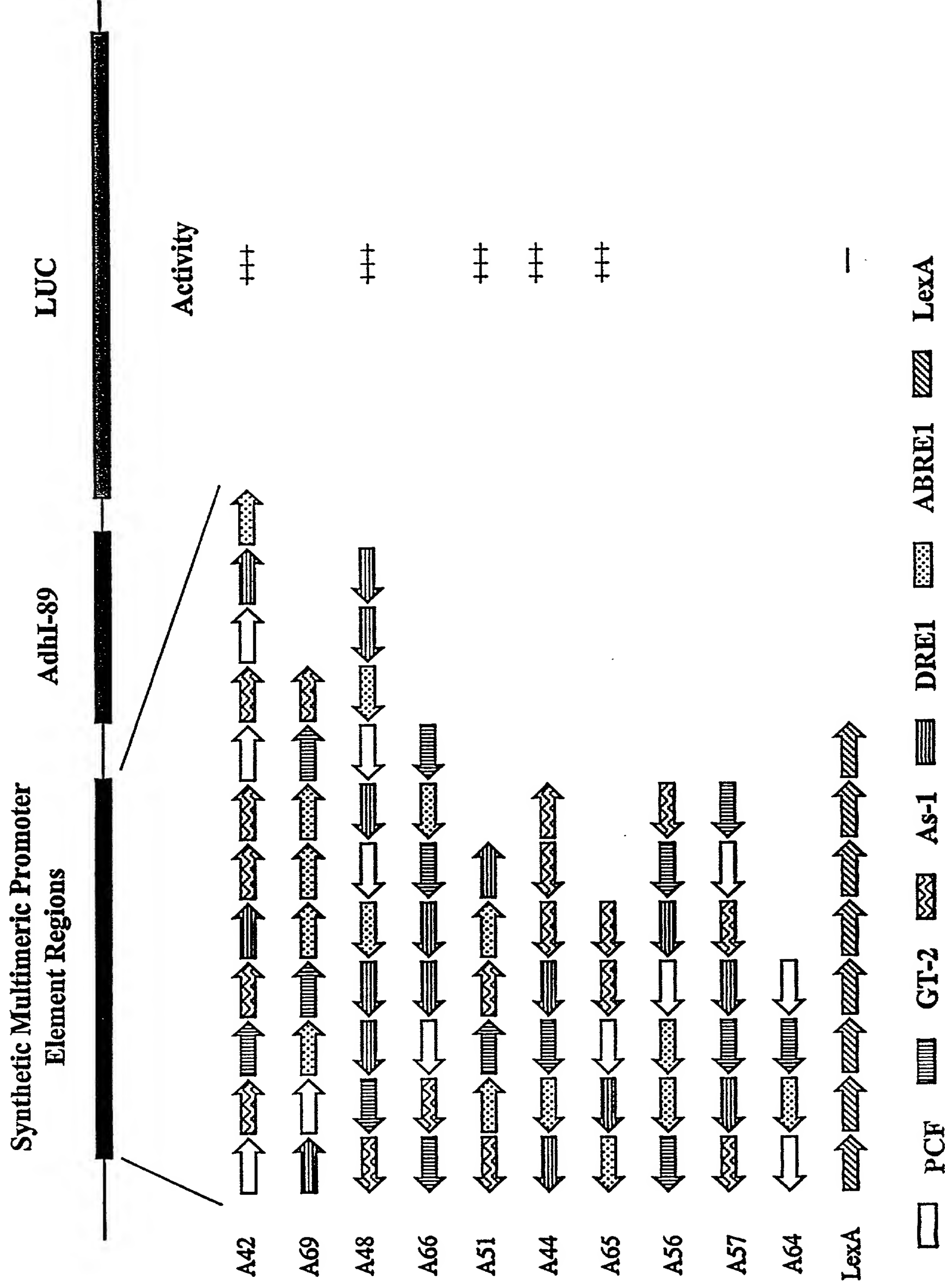


FIGURE 5



Figure 6a: Bar chart showing Adh Intron Plus Constructs (root) for three replicates (Rep1, Rep2, Rep3) across various constructs (LexA, A18, A23, A26, A15, A24, A22, A8). The y-axis ranges from 0 to 3000. Rep1 is represented by light gray bars, Rep2 by dark gray bars, and Rep3 by white bars.

### Adh Intron Plus Constructs (root)

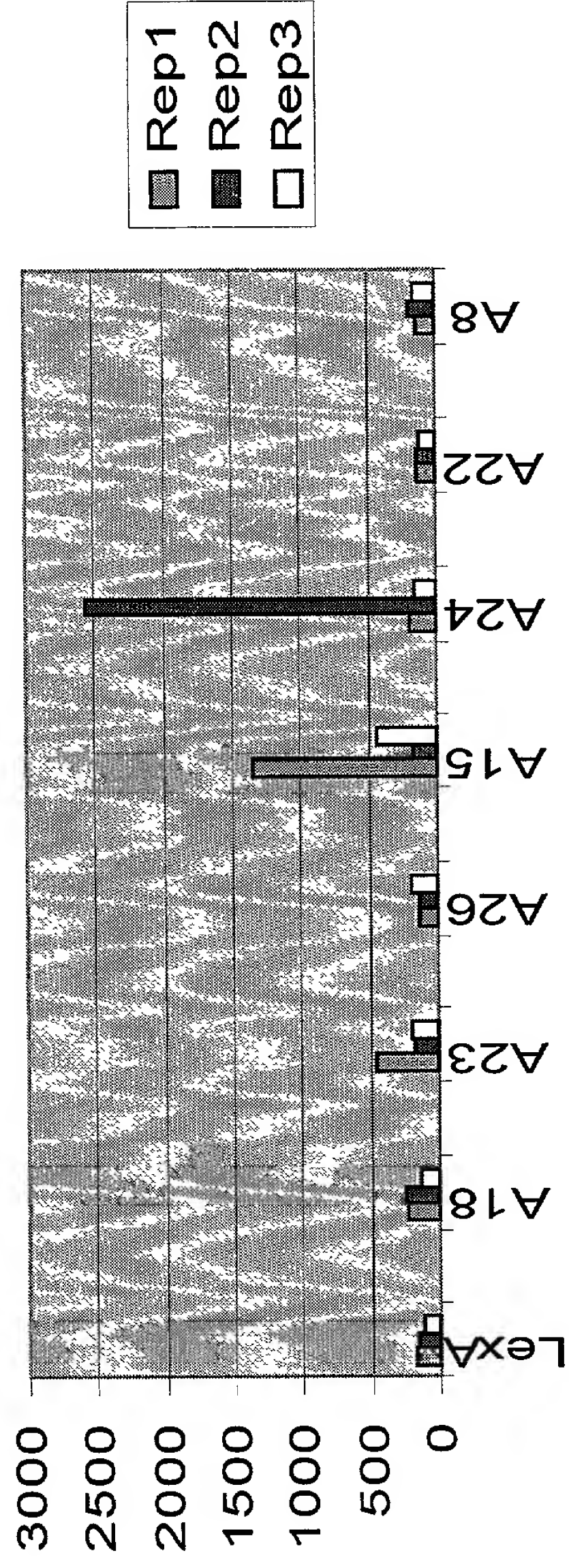


Figure 6a

### Adh Intron Plus Constructs (shoot)

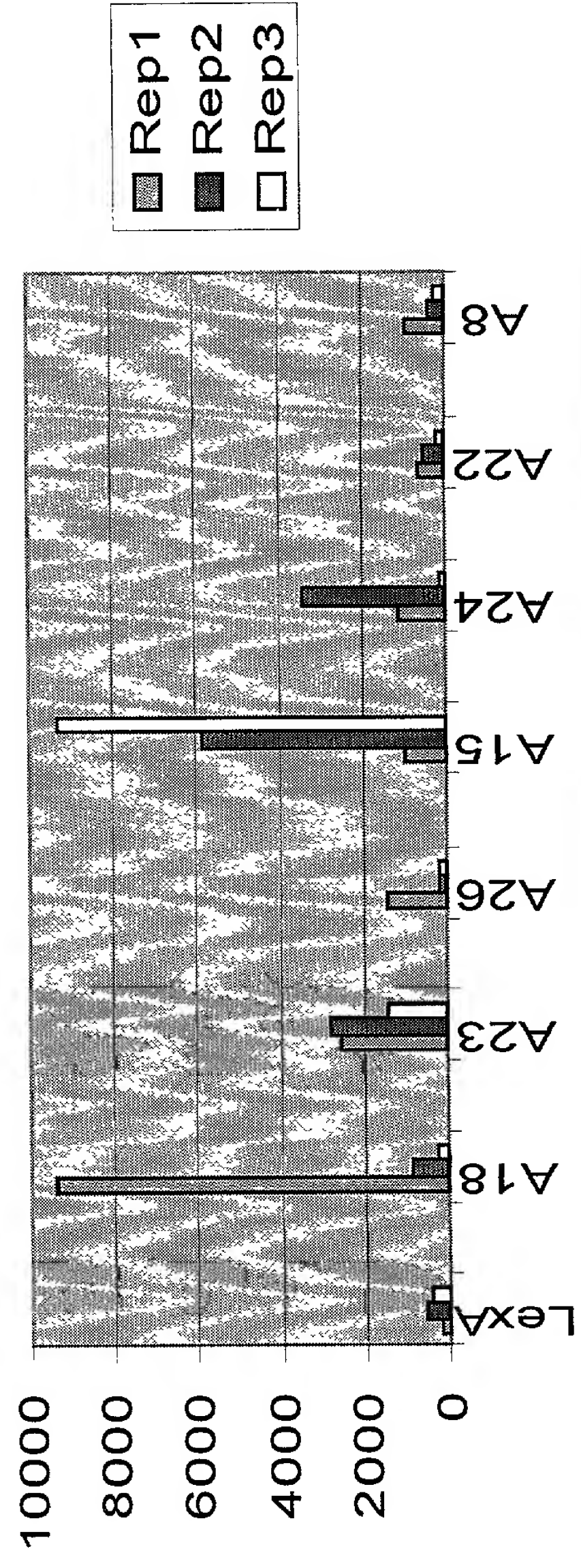


Figure 6b

Figure 6c

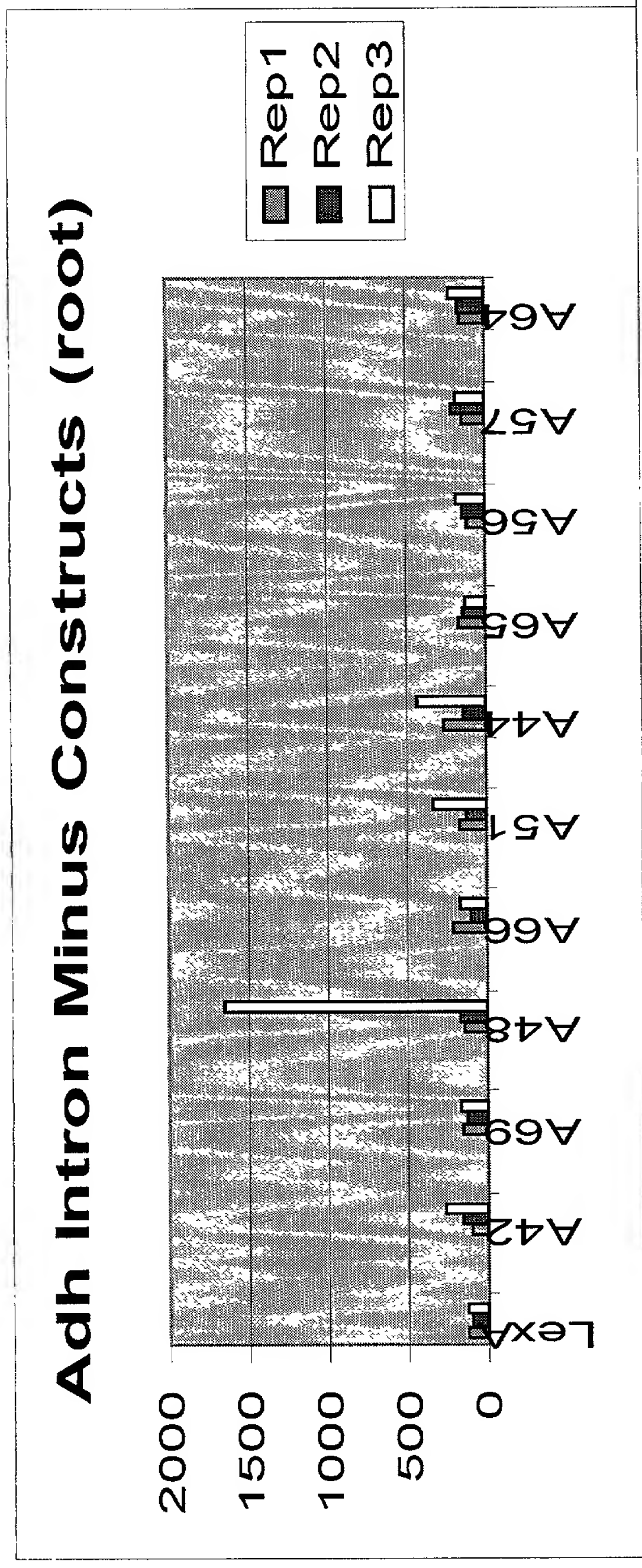


Figure 6c

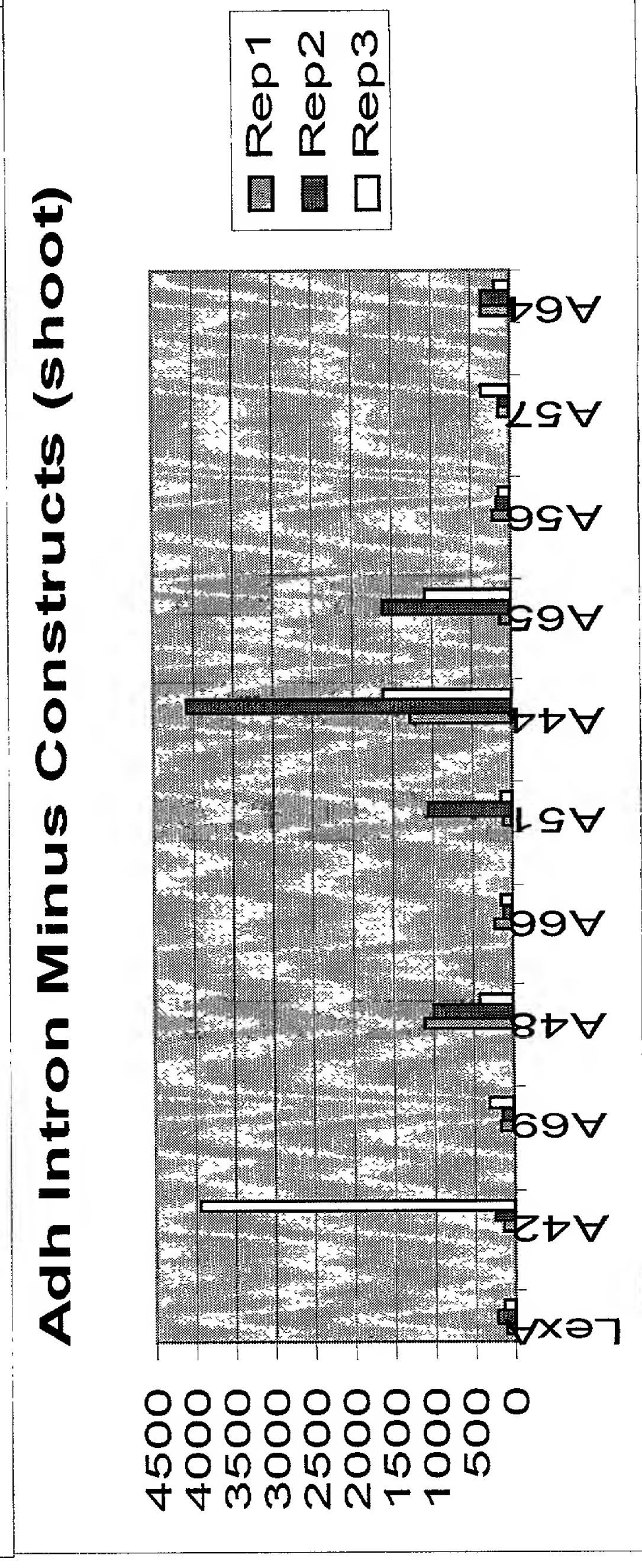


Figure 6d

A15 (PHP14147) 413bp

GT-2 ABRE1  
TAGGTTAATTTATTGGGCGGTAATTATAGCTTCGAGAAGAACCGAGACGTGGCGGGCTAG  
ABRE1 GT-2  
CTTCGAGAAGAACCGAGACGTGGCGGGCTAGCTAGGTTAATTATTGGCGGGTAATTATAG  
AS-1 GT-2  
CTCCACTGACGTAAGGGATGACGCACAATTAGCTAGGTTAATTATTGGCGATAATTATAG  
GT-2 DRE1  
CTAGGTTAATTATTGGCGGTAATTATAGCATATCATACCGACATCAGTTTAGCTAGGTTA  
GT-2 DRE1 DRE1  
ATTATTGGCGGTAATTATAGCATATCATACCGACATCAGTTTAGCATATCATACCGACAT  
AS-1 DRE1  
CAGTTTAGCTCCACTGACGTAAGGGATGACGCACAATTAGCATATCATACCGACATCAGT  
DRE1 ABRE1  
TTAGCATATCATACCGACATCAGTTTAGCTTCGAGAAGAACCGAGACGTGGCG

FIGURE 7



A18 (PHP14148) 392bp

DRE1 ABRE1  
GCTAAACTGATGTCGGTATGATATGCTAGCCCGCCACGTCTCGGTTCTTCTCGAAGCTAAACTGA  
DRE1 AS-1 ABRE1  
TGTCGGTATGATATGCTAATTGTGCGTCATCCCTTACGTCAGTGGAGCTAGCCCGCCACGTCTCG  
DRE1 GT-2  
GTTCTTCTCGAAGCTAAACTGATGTCGGTATGATATGCTATAATTACCGCCAATAATTAACCTAG  
AS-1 DRE1  
CTAATTGTGCGTCATCCCTTACGTCAGTGGAGCTAAACTGATGTCGGTAGATATGCTAATACGGG  
PCF PCF  
CCCACCTACGGGCCCACCTCGGCTAATACGGGCCCACCTACGGGCCCACCTCGGCTAAACTGATG  
DRE1 AS-1 DRE1  
TCGGTATGATATGCTAATTGTGCGTCATCCCTTACGTCAGTGGAGCTAAACTGATGTCGGTATGA  
TA

FIGURE 8

A23 (PHP14149) 314bp

DRE1 DRE1 AS-1  
TAGCATATCATACCGACATCAGTTTAGCATATCATACCGACATCAGTTTAGCTCCACTGACGTAA  
PCF1 ABRE1  
GGGATGACGCACAATTAGCCGAGGTGGGCCCCGTAGGTGGGCCCCGTATTAGCTTCGAGAAGAACCG  
PCF1 ABRE1  
AGACGTGGCGGGCTAGCCGAGGTGGGCCCCGTAGGTGGGCCCCGTATTAGCTTCGAGAAGAAGTGTAG  
DRE1 GT-2  
ACGTGGCGGGCTAGCATATCATACCGACATCAGTTTAGCTAGGTTAATTATTGGCGGTAATTATA  
GT-2 ABRE1  
GCTAGGTTAATTATTGGCGGTAATTATAGCTTCGAGAAGAACCGAGGACGTGGC

FIGURE 9

A24 (PHP14150) 278bp

ABRE1 ABRE1 GT-2  
TAGCTTCGAGAAGACGTGGCGGGCCGCCACGTCTCGGTTCTTCTCGAAGCTATAATTACCGCCAA  
GT-2 GT-2  
TAATTAACCTAGCTATAATTACCGCCAATAATTAACCTAGCTATAATTACCGCCAATAATTAACC  
DRE1 DRE1 DRE1  
TAGCTAAACTGATGTCGGTATGATATGCTAAACTGATGTCGGTATGATATGCTAAACTGATGTCG  
DRE1 ABRE1  
GTATGATATGCTAAACTGATGTCGGTATGATATGCTAGCCCGCCACGTCTCGGTTCTTCTCGAAG  
PCF  
CTAATACGGGCCCACCTA

FIGURE 10

A42 (PHP14151) 348bp

PCF AS-1  
CGAGGTGGGCCCCGTAGGTGGGCCCCGTATTAGCTCCACTGACGTAAGGGATGACGCACAATTAGCT  
GT-2 AS-1  
AGGTTAATTATTGGCGGTAATTATAGCTCCACTGACGTAAGGGATGACGCACAATTAGCATATCA  
DRE1 AS-1 AS-1  
TACCGACATCAGTTTAGCTCCACTGACGTAAGGGATGACGCACAATTAGCTCCACTGACGTAAGG  
PCF AS-1  
GATGACGCACAATTAGCCGAGGTGGGCCCCGTAGGTGGGCCCCGTATTCCACTGACGTAAGGGATGA  
PCF DRE1  
CGCACAATTAGCCGAGGTGGGCCCCGAGGTGGGCCCCGTATTAGCATATCATACCGACATCAGTTTA  
ABRE1  
GCTTCGAGAAGAACCGAGTCGAG

FIGURE 11

A44 (PHP14152) 198bp

DRE1

ABRE1

TAAACTGATGTCGGTATGATAATGCCAACCCGGCAACGTCCCGGTTCTTCTCGAAGCTATAATTA

GT-2

DRE1

As-1

CCGCCAATAATTAACCTAGCTAAACTGATGTCGGTATGATATGCTAATTGTGCGTCATCCCTTAC

As-1

As-1

GTCAGTGGAGCTAATTGTGCGTCATCCCTTACGTCAGTGGAGCTCCACTGAACGTAAGGGATGAC

GTC

FIGURE 12



A48 (PHP14153) 302bp

AS-1		GT-2
TTGTGCGTCATCCCTTACGTCAGTGGAGTAATTACCGCCAATAATTAACCTAGCTAAACTGATGT		
DRE1	DRE1	ABRE1
CGGTATGATATGCTAAACTGATGTCGGTATGATATGCTAGCCCGCCACGTCTCGGTTCTTCTCGA		
PCF		DRE1
AGCTAATACGGGCCCCACCTACGGGCCCCACCTCGGCTAAACTGATGTCGGTATGATATGCTAATAC		
PCF		ABRE1
GGGCCCCACCTACGGGCCCCACCTCGGCTAGCCCGCCACGTCTCGGTTCTTCTCGAAGCTAAACTGA		
DRE1	DRE1	
TGTCGGTATGATATGCTAAACTGATGTCGGTATGATATGCTA		

FIGURE 13

A51 (PHP14154) 157bp

AS-1 ABRE1  
GTGCGTCATCCCTTACGTCAGTGGAGCTTCGAGAAGAACCGAGACGTGGCGGGCTAGCTAGGTTA  
GT-2 AS-1 ABRE1  
ATTATTGGCGGTAATTATAGCTCCACTGACGTAAGAGCTTCGAGAAGAACCGAGACGTGGCGGGC  
DRE1  
TAGCATATCATACCGACATCAGTTTAG

FIGURE 14